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Rogan et al. (43) **Pub. Date: Dec. 26, 2019**(54) **METHOD OF VALIDATING MRNA  
SPLICING MUTATIONS IN COMPLETE  
TRANSCRIPTOMES**(71) Applicant: **Cytognomix Inc**, London (CA)(72) Inventors: **Peter Keith Rogan**, London (CA);  
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(2013.01)(57) **ABSTRACT**

A method is described for the automatic validation of DNA sequencing variants that alter mRNA splicing from nucleic acids isolated from a patient or tissue sample. Evidence of a predicted splicing mutation is demonstrated by performing statistically valid comparisons between sequence read counts of abnormal RNA species in mutant versus non-mutant tissues. The method leverages large numbers of control samples to corroborate the consequences of predicted splicing variants in complete genomes and exomes for individuals carrying such mutations. Because the method examines all transcript evidence in a genome, it is not necessary a priori to know which gene or genes carry a splicing mutation.